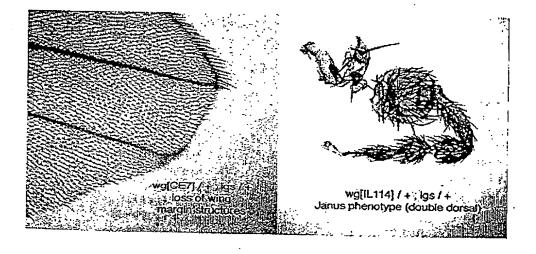
wild type sev-wg sev-wg, lgs<sup>\$17</sup>/+

В



C



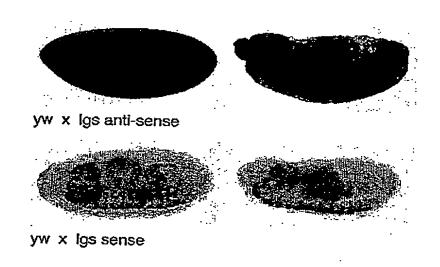
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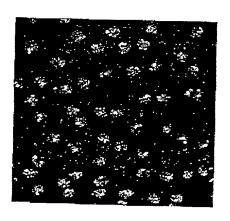
## Figure 2: legless

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NAQCQELIOFTHNALKSTAC	1392
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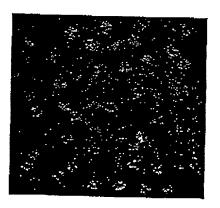


Figure 4

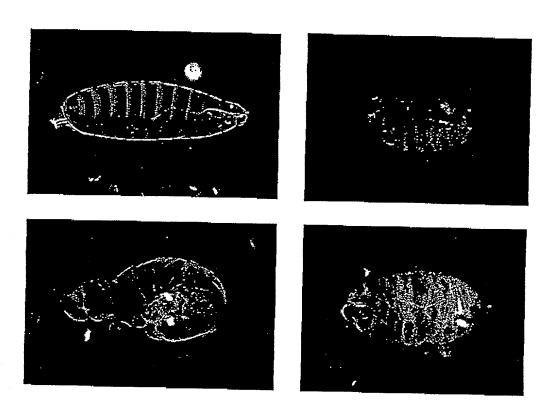
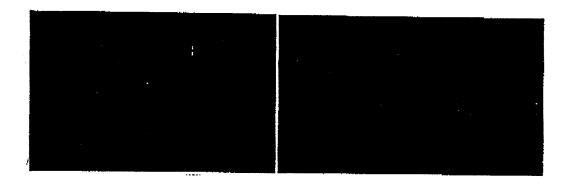


Figure 5

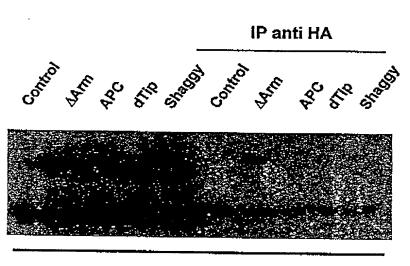
Α

EGFP-Lgs

EGFP-Lgs + pcDNA3-Arm-NLS



В



Anti-EGFP

5C

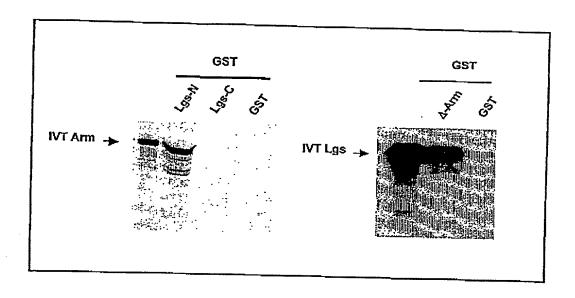
BAIT fusions: pLex Lgs BCL9 BCL9 Dco+ Δß-Cat ΔArmC Pan 1-1464 199-392 1-1426 lgs364-555 PREY fusions: pJG4-5 lgs1-385 lgs1-732 lgs364-1090 lgs726-1464 lgs1-1464 BCL9 199-392 BCL91-1426 Dco+ DAxin **∆Arm**¢ B-Cat opposities. Pan pJG4-5

+: interaction seen in yeast two-hybrid assay

numberings refer to amino acid positions.

<sup>-:</sup> no interaction seen in yeast two-hybrid assay n.d.; not done

5 D



5E

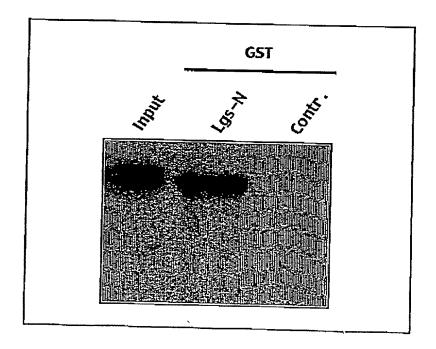
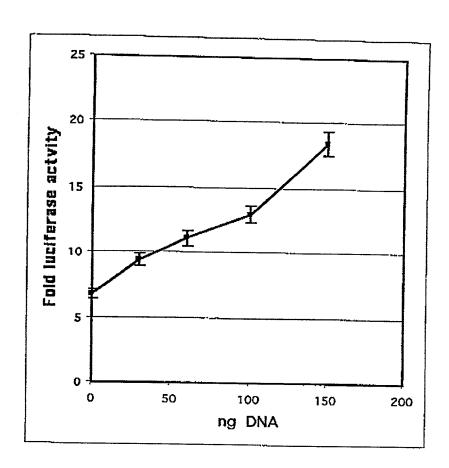
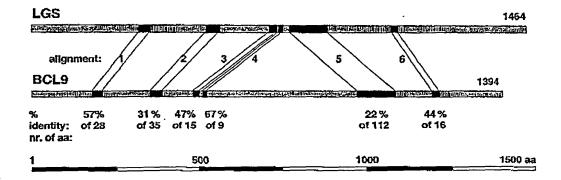


Figure 6



## A



### **7B**

### Sequence homology domain 1: 57.1% identity in 28 22

	320	330	340
igs	IFVFSTQ	Lankgaesvi	SGQFQTTIAYH
	::::.		:: .:::
BCL9	VYVFSTE	MANKAAEAVI	KGQVETIVSFH
	180	190	200

#### Sequence homology domain 2: 31.4% identity in 35 aa

	520	530	540	
LGS	ENLTPQQR	QHREEQLAK	ikkm <u>nofl</u> f	PENENSVGA
1	:	.::: :	<b></b> ::	i , .:I
BCL9	DGLSQEQL	PHRERSLQT	LRDIORMLE	PDEKEFTGA
ł	350	360	370	380

### Sequence homology domain 3: 46.7% identity in 15 aa

	710	720
LGS	OMEWS	CIQHQFFEER
	*	
ECT3	QIAWL	OLOOELAEEK
1	470	480_

### Sequence homology domain 4: 66.6% identity in 9 aa

	760		 	·—	· ·	
LGS	LQGPPPPYH					
1	::::::					
BCL9	VRGPPPPYQ					
	520		 			

### Sequence homology domain 5: 22.3% identity in 112 aa

	770	780	790	800	810	820	
LGS	SASVPI	atospnpssp	nnlslpspri	MAAVMGLPIN	SPSMDGTGSL	SGSVPQANTSTVQA	
BCL9						SKFAMPSSTPLYHD	
	970	980	990	1000	1010	1020	
	830	840	850	860	870		
LGS	GTTTVL	SANKNCFQAL	TPSPSNQNR	erinigessyl/i	HNLSSNPSTP	LSHLSP	
BCL9				rgyginigni Pgyginigni			
	1030	1040	1050	1060	1070		

### Sequence homology domain 6: 43.8% identity in 16 a2

	1080	
LGS	NPKMCVAGGPNGPPGF	
l	: .:::::: .:	
BCL9	DAALCKPGGPGGPDSF	
L	1190 1200	

#### Α

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA TGTCCCCATCTGGAAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT AAACAGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA GAGTGGGGCCATACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG GGCTGAAGAATGGGCCTGGAAATGGTGCCAAGGGCAAGGGGAAAAGGGAG CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC AGGATTCCCAGCACACACACACTCGATGACCCCATCAAATGCTACAGCC CCCAGGTCTTCTACCCCCTCCCATGGCCAAACTACTGCCACAGAGCCCCAC ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAAACTATC GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC TCCCACACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAGCC TGCCGCACCCCCACGTCCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA AACTGATTCCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA GATGGTACTGGGCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCTCCGCCTC CACCAGTGTCCAGTGGCGAGCCCCCCCCCCCCCGGGAGAGAATCCCGATGGC CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAAACTCTCAG AGATATCCAGCGCATGCTTTTTCCTGATGAGAAAGAATTCACAGGAGCAC AAAGTGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG TAAGGGACCTGGGCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG GACATAGAGATGTACCCTTTTCTCCAGATGAAATGGTTCCACCTTCTATG AACTCCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCCTCCAGGACATG ATGCTCCATCAGCACGGGCTCGGGGAGTCGTCCGAGGACCCCCCCTCC ATACCAGATGACCCCTAGTGAAGGCTGGGCCACCTGGGGGGTACAGAGCCAT TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCCGAGGGCCATGGCT CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCCAACCCTGCATCTA GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA GATGGTCGAAATTTTCCTCCTGGCCAGGGCATTTTCAGCGGTCCTGGCCG AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCCAGGGATGGCCATGGAA GGCATCAGGOCCAGCATGAGATGAACAGGATGATTCCAGGCTCCCAGCG CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

Konrad BASLER et al "A NEW ESSENTIAL..."
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:Figure 8A

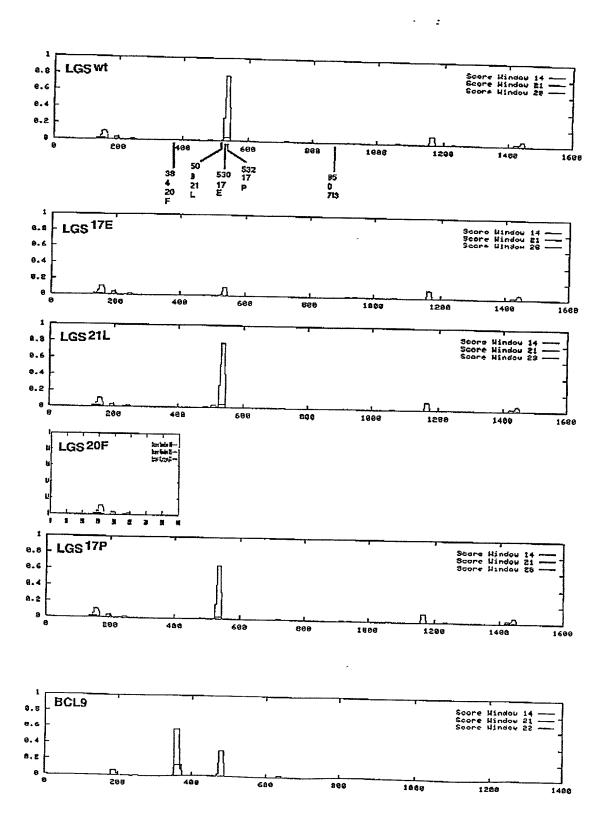
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Figure 8B

В

MHSSNPKVRSSPSGNTQSSPKSKQEVMVRPPTVMSPSGNPQLDSKFSNQG KQGGSASQSQPSPCDSKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRF RSISADSFDQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA PRSSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKGQVETI VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ NTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG LSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGGPQQNPGVLDGPQK KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPQGHRDVPFSPDEM1/PPSM NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM MVHQHGPRGVVRGPPPPYQMTPSEGWAPGGTEPFSDGINMPHSLPPRGMA PHPNMPGSQMRLPGFAGMINSEMEGPNVPNPASRPGLSGVSWPDDVPKIP **DGRNFPPGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME** GIRPSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGPLSPSRGDFPKGIPPQ MGPGRELEFGMVPSGMKGDVNLNVNMGSNSQMIPQKMREAGAGPEEMLKL RPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNL REPIGPDORTNSRLSHMPPLPLNPSSNPTSLNTAPPVORGLGRKPLDISV AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA AAASIKSPPVI.GSAAASPVHLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT LSONPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM NNMPGMG!NTQNPRISGPNPVVPMPTLSPMGMTQPLSH\$NQMPSPNAVGP NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPQGRMGFPQGFPPVQSPPQQ VPFPHNGPSGGQGSFPGGMGFPGEGPLGRPSNLPQSSADAALCKPGGPGG PDSFTVLGNSMPSVFTDPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ YFPRGEVPGPKQPQGPGPGFSHMQGMMGEQAPRMGLALPGMGGPGPVGTP DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN PAAAVGMIPGKDRGPAGLYTHPGPVGSPGMMSMQGMMGPQQNIMIPPQM RPRGMAADVGMGGFSQGPGNPGNMMF\*

Figure 9



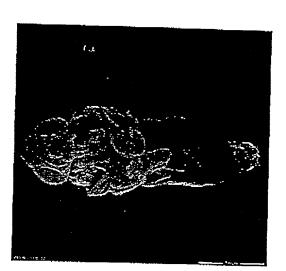
#### A

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#### В

**FKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE** LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP GGDMGQQMNMMIQRLGQDSLTPEQVAWRKLQEEYYEEKRRKEEQIGLHGS RPLQDMMGMGGMMVRGPPPPYHSKPGDQWPPGMGAQLRGPMDVQDPMQLR GGPPFPGPRFPGNQIQRVPGFGGMQSMPMEVPMNAMQRPVRPGMGWTEDL PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR PLCMAGSGMGQSMEMERMMQAHRQMDPAMFPGQMAGGEGLAGTPMGMEFG GGRGLLSPPMGQSGLREVDPPMGPGNLNWNMNVNMNMNMNLNVQMTPQQQ MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP PLNMNSSTTLSNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI ATSDDELLPDRPLLPPPPPPQGSGPGGPDSLNAPCGPVPSSSQMMPFPPR LOOPHGAMAPTGGGGGGPGLOOHYPSGMALPPEDLPNOPPGPMPPQQHLM GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPGQQ GDRPLVWIPGTRAMAPAQRCPLCRQTFFCGRGHVYSRKHQRQLKEALER LLPQVEAARKAIRAAQVERYVPEHEROCWOLOCGCEVREHLSHGNLTVLY **GGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG** LDSYEEKEDKYIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPHT TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD DTVLGVKLSIANYDL

A



В

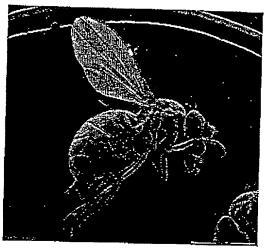
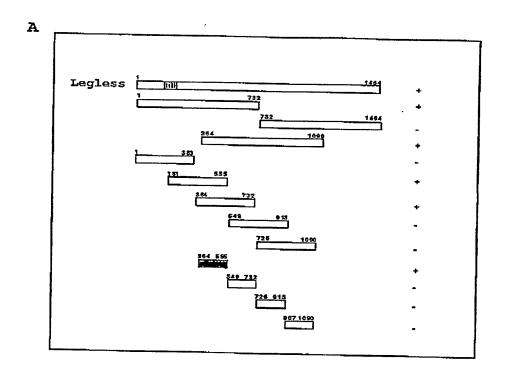
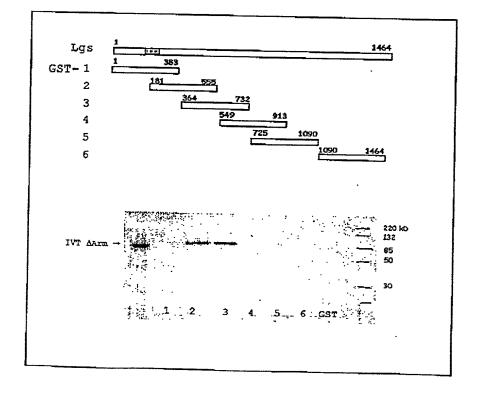
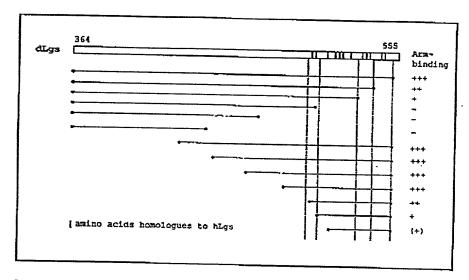


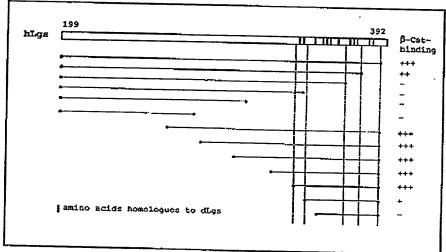
Figure 12





## Figure 12B

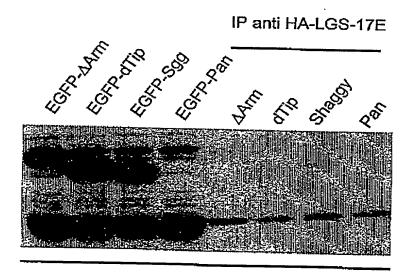




# Figure 12C

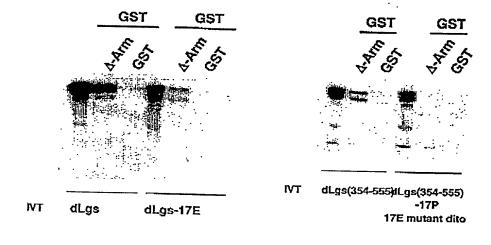
•	hı vikro interaction
N 1294567500000000000000000000000000000000000	++
	++
C C	•
N ESSE SES SES SES SES SES SES SES SES S	++
N 1 23 4 5 6 7 A	+++
N = = = = = = = = = = = = = = = = = = =	+++
N E E E E E E	++
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	++
1 23 4 5 6 7 8	+++
125456	+++
1254	4-4
<b>0</b> 0	-
e de la companya de l	(+)
	(+) (-)
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A



Blot anti-EGFP

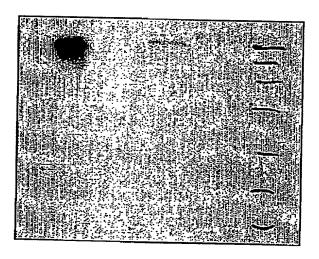
В



C

 $\begin{array}{ccc} \text{IVT} & \text{GST} & \text{GST-} \\ \text{input} & \beta\text{-Cat} \end{array}$ 

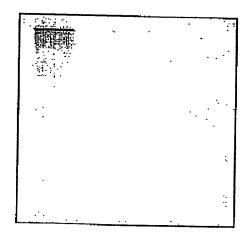
IVT-hLgs →

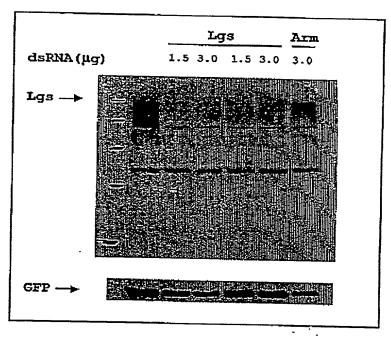


 $\mathbf{D}$ 

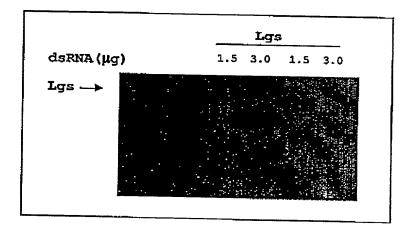
 $\begin{array}{ccc} \text{IVT} & \text{GST} & \text{GST-} \\ \text{input} & \beta\text{-Cat} \end{array}$ 

 $IVT-hLgsdn \rightarrow$ 



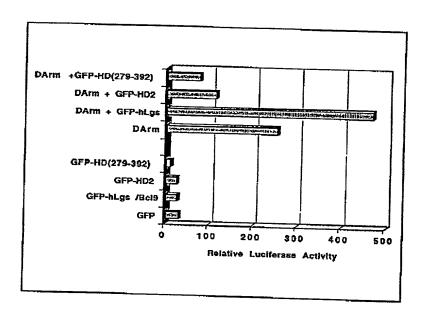


pMT-EGFP (µg) 1.5 1.5 1.5 1.5 1.5



pMT-dLgs (μg) - 2 2 2 2 2

Ą



B

